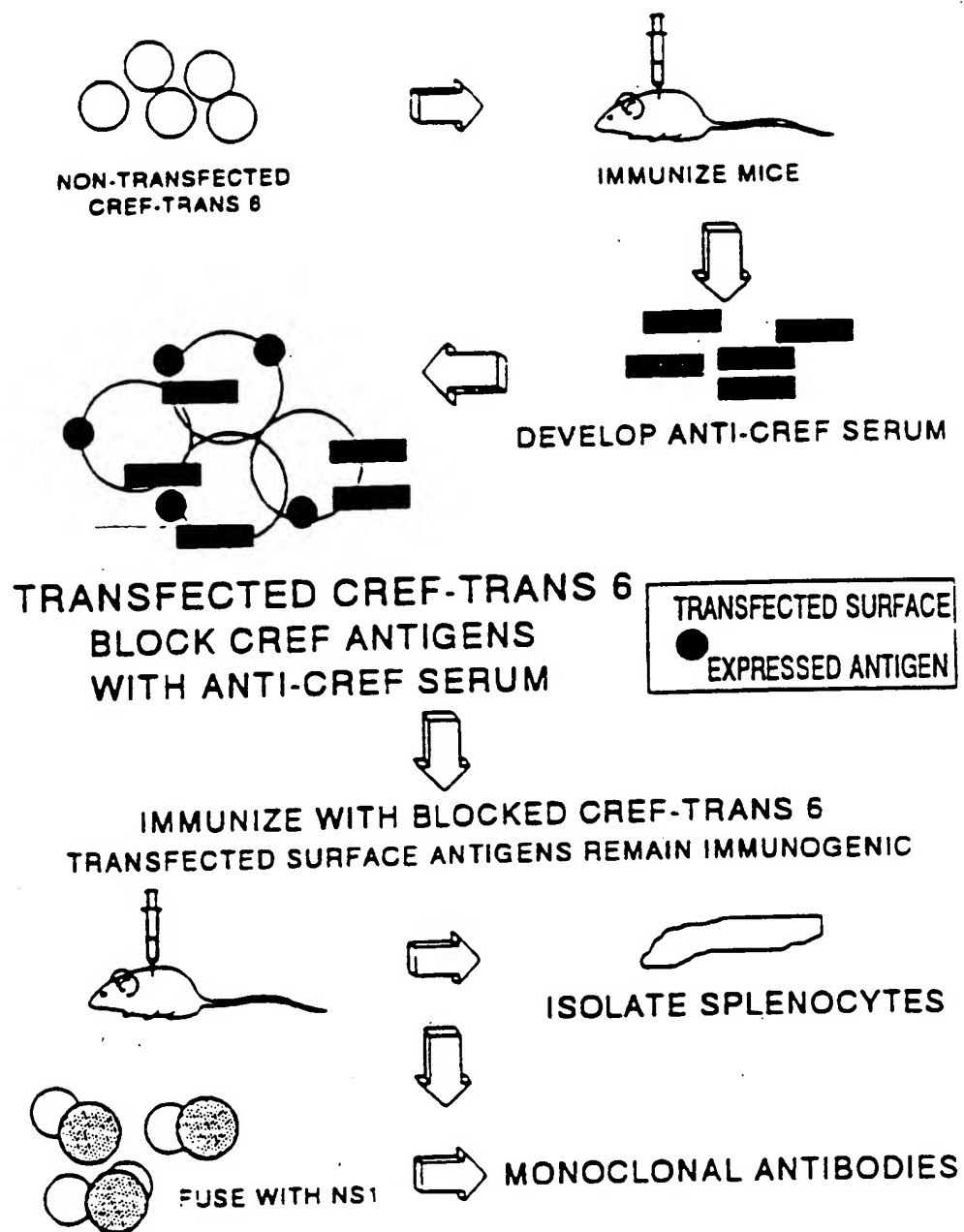


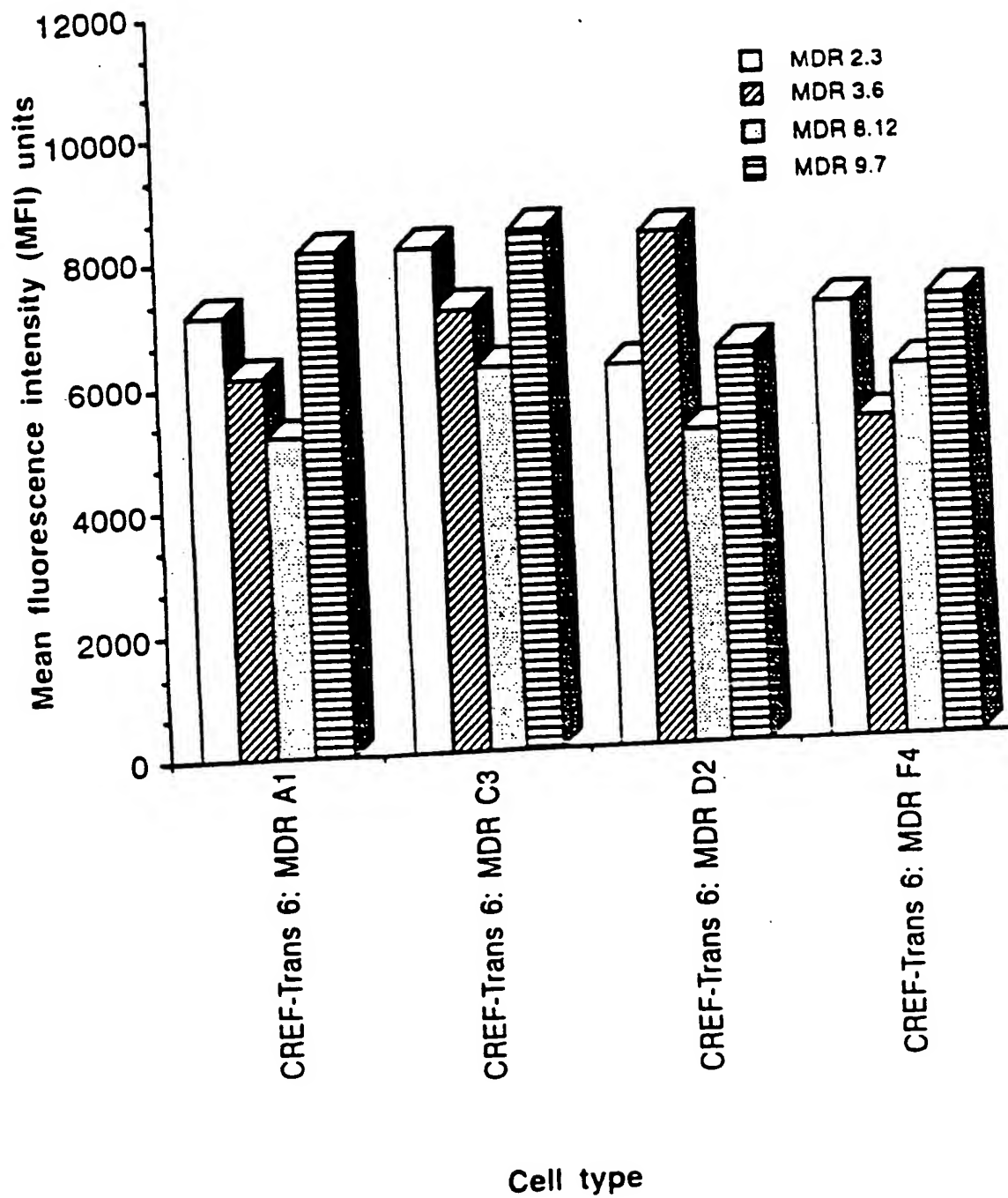
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FIGURE 1



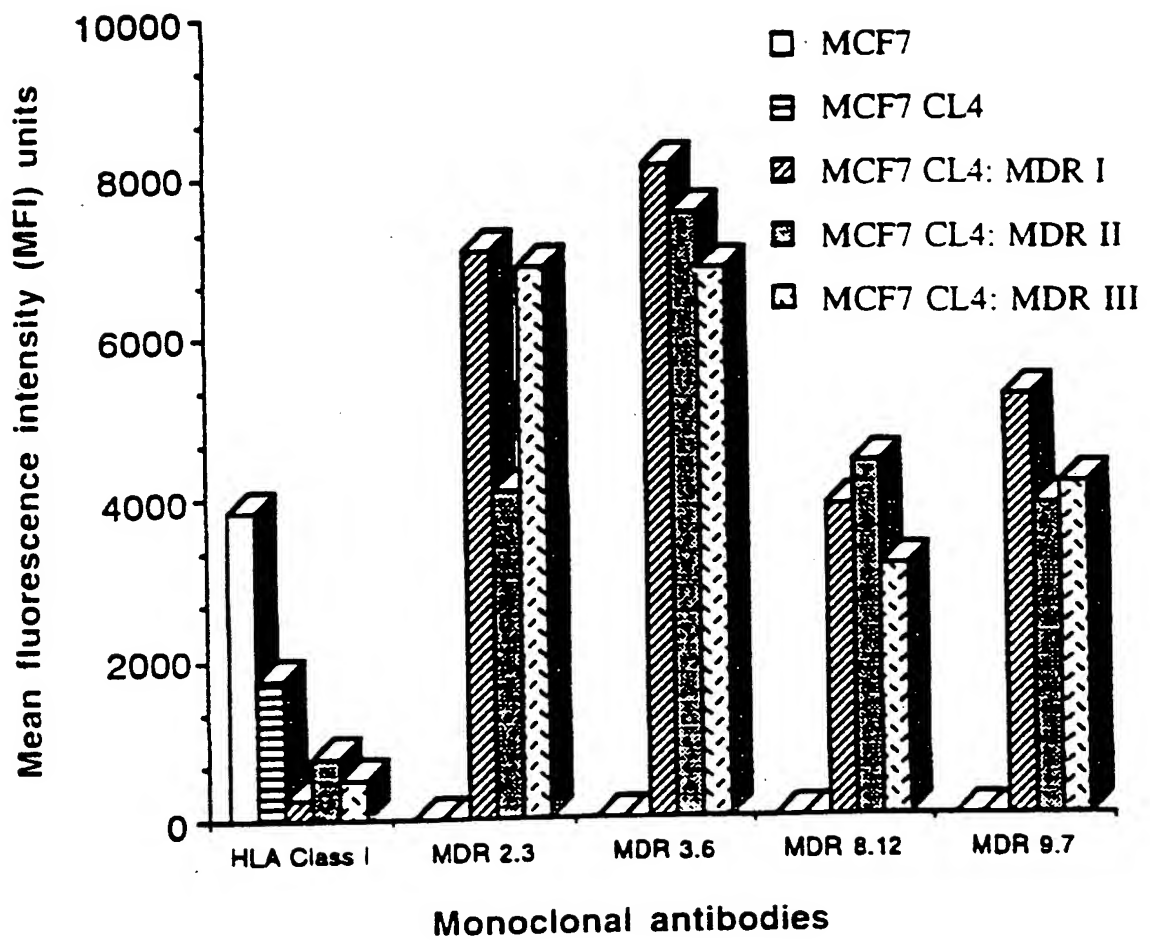
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FIGURE 2



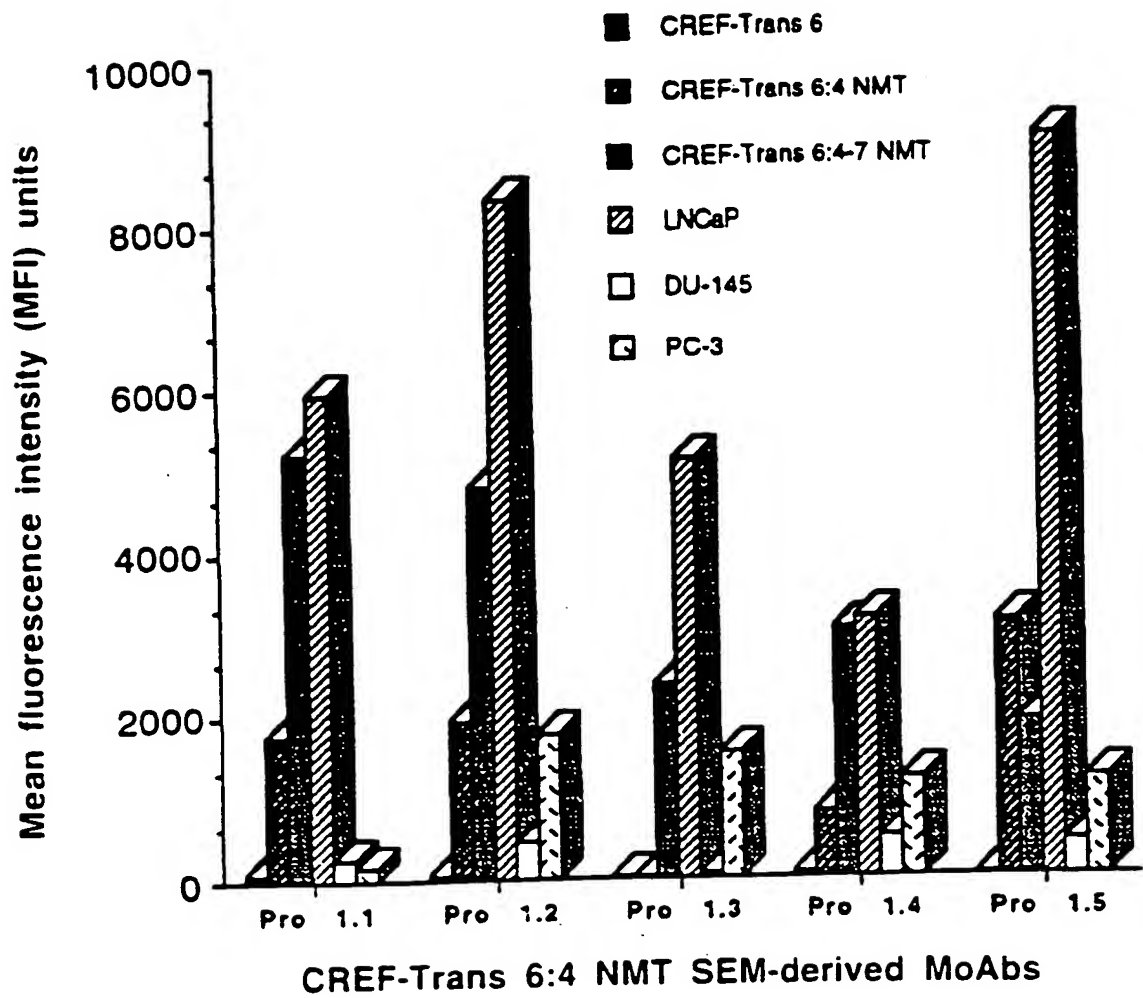
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FIGURE 3



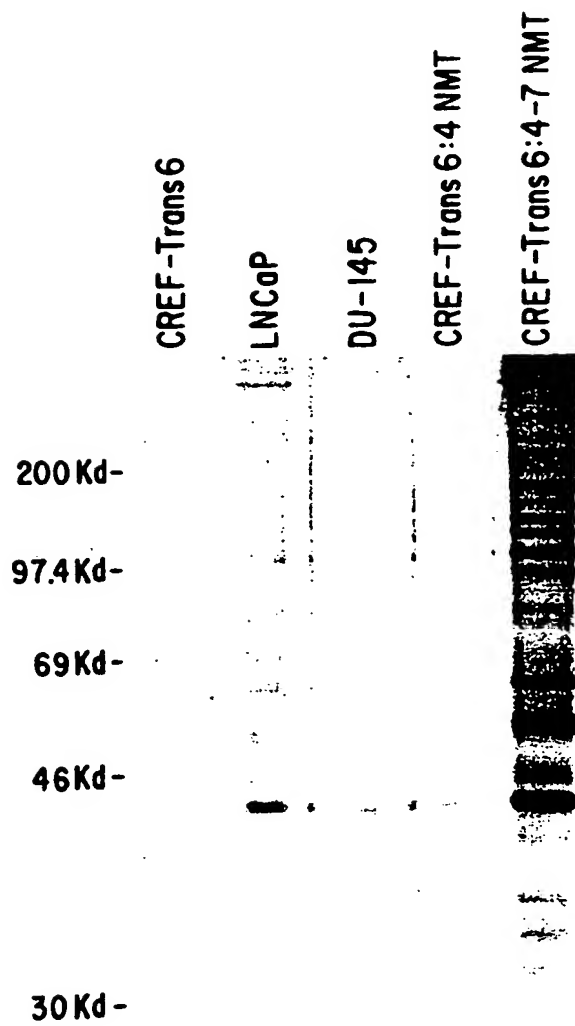
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FIGURE 4



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FIGURE 5

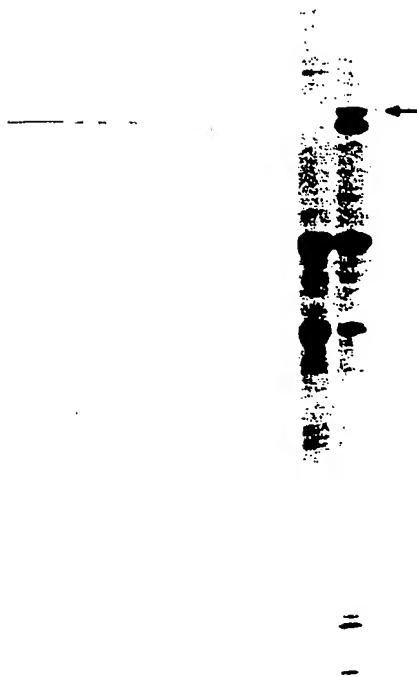


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FIGURE 6

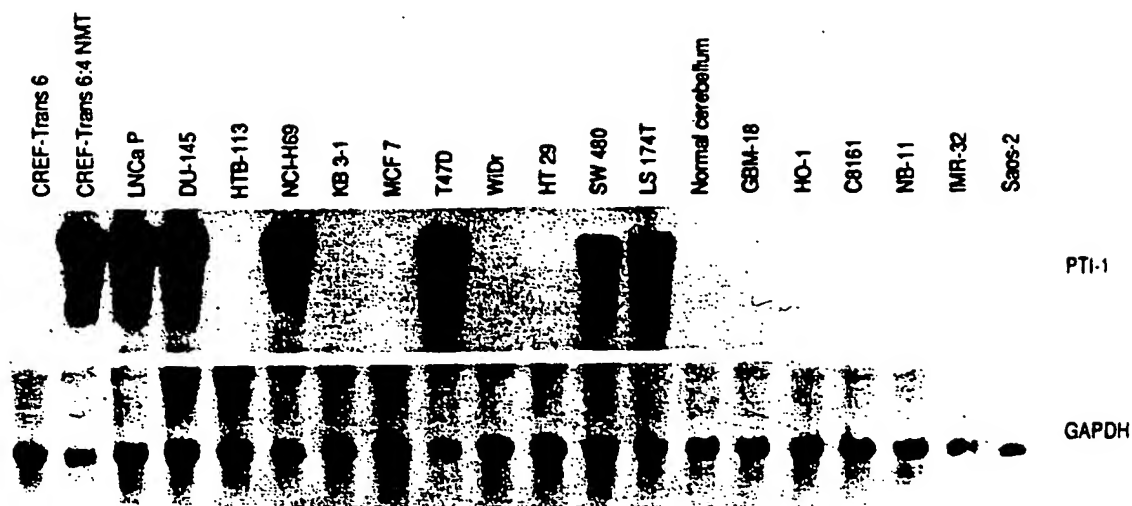
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FIGURE 7



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FIGURE 8A

1 gtatcgaatcatanaatcicatatagatglatccctgagtagggcgggcccgigaaccctcigaatcgcggccaccaccggtaaggc 90
91 taataactaatcagacaccgatagtagaacctagtaggggaaaggigaagaacccgagaggggagtagaatagattc:gaazacc 179
180 atttacttacaag:ggiccatitact:acaagtgicagagcacgitaag:gtgatggcgtagcatc:tgcatatggggccggcgag:ta:g: 271
272 taataigcaaggtaagcagaaaaagcggagccgtagggaaaccgagictgaatagggcgactitagtatatggcatatacccgaa2: 361
362 caggtagatctatccatgagcagggtgaagcttaggtaaaactaagtgaggaccgaaccgtagtagctaaaaagtgcccggaaggact: 451
452 gtagatagtggtgaatccaatcgaacctggagatagctggitctctcgaatagcttagggctagcgtatagtagtattgtaaatgggg 543
544 tagagcacigaatgtggaatggcgcatcagctgactgactataatcaaacctccgaataccattaaaattaagc:ATG CAG TCG 629
M Q S
630 GAA CGT GGT ATC ACC ATT GAT ATC TCC TTG TGG AAA TTT GAG ACC AGC AAG TAC TAT 686
E R G I T I D I S L W K F E T S K Y Y
687 GTG ACT ATC ATT GAT GCC CCA GGA CAC AGA GAC TTT ATC CAA AAC ATG ATT ACA GG 742
V T I I D A P G H R D F I Q N M I T G
743 G ACC TCT CAG GCT GAC TGT GCT GTC CTG ATT GTT GCT GCT GGT GTT GGT GAA TTT GAA G 801
G S Q A D C A V L I V A A G V G E F E
802 CT GGT ATC TCC AAG AAT GGG CAG ACC CGA CAG CAT GCC CTT CTG GCT TAC ACA CTG GG 855
A G I S K N G Q T R E H A L L A Y I L G
859 T GTG AAA CAA CTA ATT GTC GGT GTT AAC AAA ATG GAT TCC ACT GAG CCA CCC TAC 914
V K Q L I N G V N K M D S T E P P Y
915 AGC CAG AAG AGA TAT GAG GAA ATT GTT AAG GAA GTC AGC ACT TAC ATT AAG AAA 968
S Q K R Y E E I V K E V S T Y I K K
969 ATT GGC TAC AAC CCC GAC ACA GTA GCA TTT GTG CCA ATT TCT GGT TGG AAT GGT GAC 1025
I G Y N P D T V A F V P I S G W N G D
1026 AAC ATG CTG GAG CCA AGT GCT AAC ATG CCT TGG TTC AAG GGA TGG AAA GTC ACC CGT 1082
N M L E P S A N M P W F K G W K V T R
1083 AAG GAT GGC AAT GCC AGT GGA ACC ACG CTG CTT GAG GCT CTG GAC TGC ATC CTA CCA 1139
K D G N A S G T T L L E A L D C I L P
1140 CCA ACT CGT CCA ACT GAC AAG CCC TTG GGC CTG CCT CTC CAG GAT GTC TAC AAA ATT 1196
P T R P T D K P L Q L P L Q D V Y K I
1197 GGT GGT ATT GGT ACT GTT CCT GTT GGC CGA GTG GAG ACT GGT GTT CTC AAA CCC GGT 1253
G G I G T V P V G R V E T G V L K P G
1254 ATG GTG GTC ACC TTT CGT CCA GTC AAC GTT ACA ACG GAA GTA AAA TCT GTC GAA ATG 1310
M V V T F Q P V N V T T E V K S V E M
1311 CAC CAT GAA GCT TTG GGT GAA GCT CTT CCT GGG GAC AAT GTG GGC TTC AAT GTC AAG 1367
H H E A L G E A L P G D N V G F N V K
1368 AAT GTG TCT GTC AAG GAT GTT CGT CGT GGC AAC GTT GCT GGT GAC AGC AAA AAT GAC 1424
N V S V K D V R R G N V A G D S K N D
1425 CCA CCA ATG GAA GCA GCT GGC TTC CCT GCT CAG GTG ATT ATC CTG AAC CAT CCA GGC 1481
P P M E A A G F P A Q V I I L N H P G
1482 CAA ATA AGC GCC GGC TAT GCC CCT GTA TTG GAT TGC CAC ACG GCT CAC ATT GCA TGC 1538
Q I S A G Y A P V L D C H T A H I A C
1539 AAG TTT GCT GAG CTG AAG GAA AAG ATT GAT CGC CGT TCT GGT AAA AAG CTG GAA 1592
K F A E L K E K I D R R S G K K L E
1593 GAT GGC CCT AAA TTC TTG AAG TCT GGT GAT GCT GCC ATT GTT GAT ATG GTT CCT GGC 1649
D G P K F L K S G D A A I V D M V P G
1650 AAG CCC ATG TGT GTT GAG AGC TTC TCA GAC TAT CCA CCT TTG GGC GGC TTT GCT GTT 1706
K P M C V E S F S D Y P P L G Q F A V
1707 CGT GAT ATG AGA CAG ACA GTT GCG GTG GGT GTC ATC AAA GCA GTG GAC AAG AAG GCT 1763
R D M R Q T V A V G V I K A V D K K A
1764 GCT GGA GCT GGC AAG GTC ACC AAG TCT GCC CAG AAA GCT CAG AAG GCT AAA TGA 1817
A G A G K V T K S A Q K A K K K
1818 atattatccctaataccctcccccacttataatcag:ggtaggaagaccgggtcagaaac:gt:tggttcaatggccatttaagttag: 1904
1910 agtaaaagagctgggttaatgataaacaatgcacgttaaaaccttcagaaggaaaggagaatgttttgtagaccacgttggtttctttttgc 1996
1997 gtagggcagtttaagttatag:tttttaaaatcagtagtttttaatggaaacaacttgaccccccata:ttgtacagaa:tttgggaccca: 1089
2090 taaaaagggttaactgggtaaaaaaaaaaaaaa 2123

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FIGURE 8B

(E)1		MGKEKTHINIVVIGH	15
(E)16		<u>YDSGKSTTTGHLVKCGGIDKRTEKEFEKAAEMGKSEKYAWVLDKLKAER</u>	67
(P)1		MQS	3
(E)68		ERGITIDISLWKFETSKYYVTIIDAPGHRDFIKNMITGTSQADCAVLIVAAGV	120
(P)4		ERGITIDISLWKFETSKYYVTIIDAPGHRDFIQNMITGTSQADCAVLIVAAGV	56
(E)121		GEFEAGISKNGQTREHALLAYTLGVKQLVGVNKMMDSTEPYPYSQKRYEEIVKE	173
(P)57		GEFEAGISKNGQTREHALLAYTLGVKQLVGVNKMMDSTEPYPYSQKRYEEIVKE	109
(E)174		VSTYKKIGYNPDTVAFVPISGWNGDNMLEPSANMPWFKGWKVTRKDGNA	223
(P)110		VSTYKKIGYNPDTVAFVPISGWNGDNMLEPSANMPWFKGWKVTRKDGNA	159
(E)224		SGTILLEALDCILPPTPTDKPLRLPLQDVYKIGGIGTVPVGRVETGVLPKPGM	276
(P)160		SGTILLEALDCILPPTPTDKPLGLPLQDVYKIGGIGTVPVGRVETGVLPKPGM	212
(E)277		VVTFAPVNVTTTEVKSVEMHHEALSEALPGDENVGFNVKNVSVKDVRRGNV	325
(P)213		VVTFGPVNVTTTEVKSVEMHHEALGEALPGDENVGFNVKNVSVKDVRRGNV	261
(E)326		AGDSKNDPPMEAGFTAQVILNHPGQISAGYAPVLDCHTAHLACKFAELK	376
(P)262		AGDSKNDPPMEAGFTAQVILNHPGQISAGYAPVLDCHTAHLACKFAELK	312
(E)377		EKIDRRSGKKLEDGPKFLKSGDAAIVDMVPGKPMCVESFSDYPPLGRFAVRD	428
(P)313		EKIDRRSGKKLEDGPKFLKSGDAAIVDMVPGKPMCVESFSDYPPLGCTFAVRD	364
(E)429		MRQTVAVGVKA VDKKAAGAGKVTKSAQKAQKAK	462
(P)365		MRQTVAVGVKA VDKKAAGAGKVTKSAQKAQKAK	398

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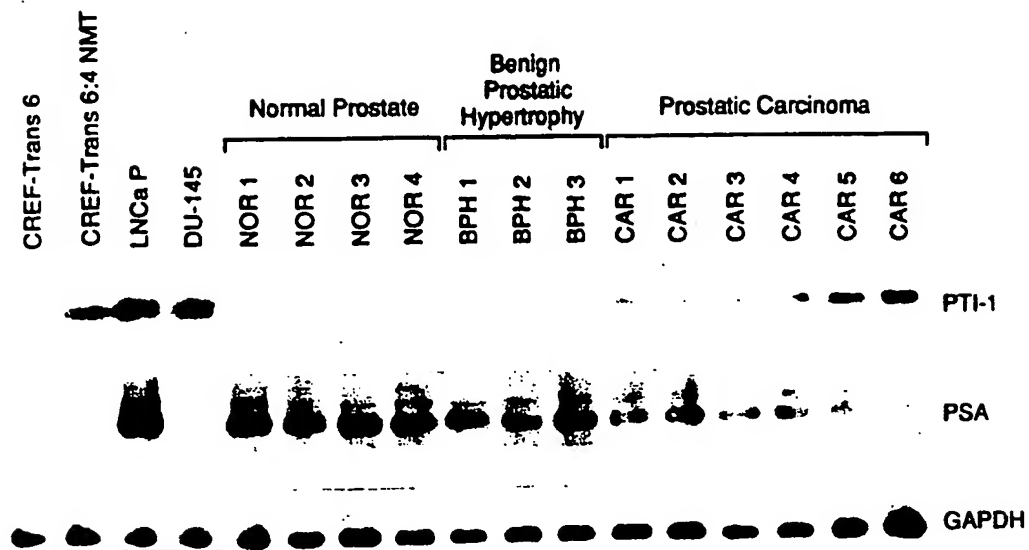
FIGURE 8C

Human EF-1 α	Amino Acid	K (100)	R (247)	A (281)	S (300)	T (341)	R (423)
	Codon	AAA	CGC	GCT	AGT	ACT	CGC
	Nucleotide	A	C	C	A	A	C

PTI-1	Amino Acid	Q (36)	G (183)	G (217)	G (236)	P (277)	C (359)
	Codon	CAA	GGC	GGT	GGT	QCT	TGC
	Nucleotide	C	G	G	G	C	T

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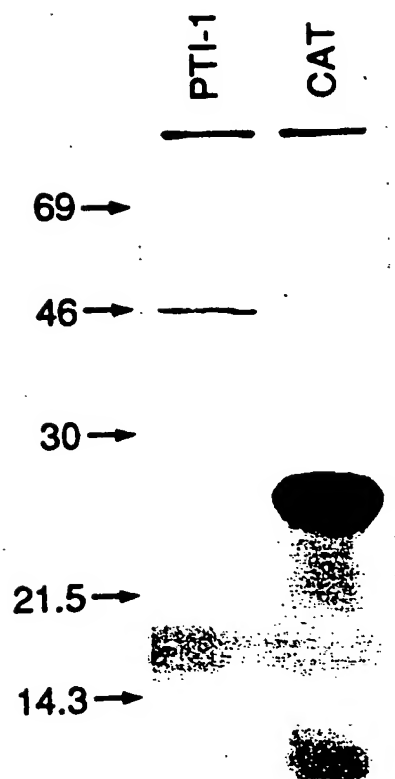
FIGURE 9



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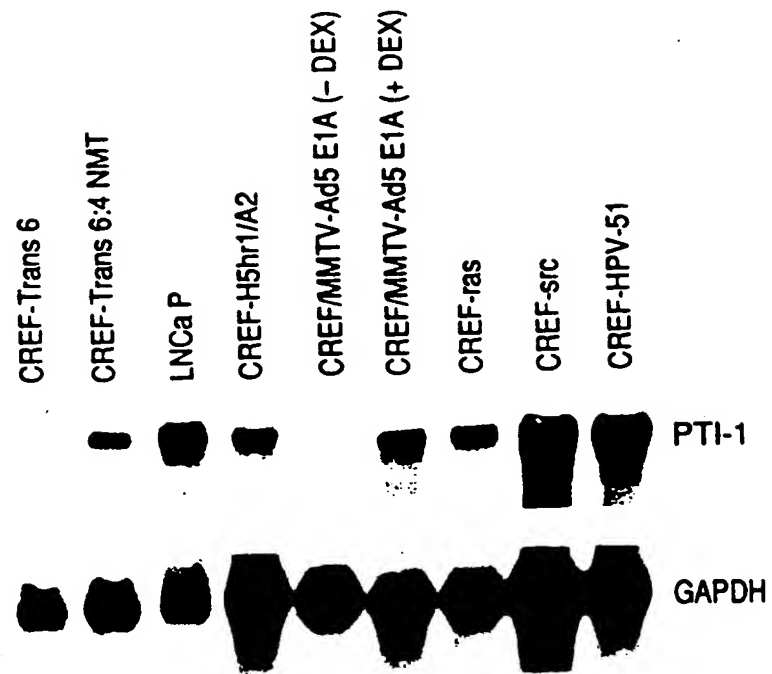
FIGURE 10



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FIGURE 11



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FIGURE 12B



FIGURE 12D



FIGURE 12A



FIGURE 12C



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FIGURE 13A

1 CGGACCGAGC TCCGTTGCAT TTTGATGAAT CCATAGTCAA ATTAGCGAGA
51 CACGTTGCGA ATTGAAACAT CTTAGTAGCA ACAGGAAAAG AAAATAAATA
101 ATGATTTTCGT CAGTAGTGGC GAGCGAAAGC GAAAGAGCCC AAACCTGTAA
151 AGGGGGGTTG GTAGGACATC TTACATTGAG TTACAAAATT TTATGATAGT
201 AGAAGAAGTT GGGAAAGCTT CAACATAGAA GGTGATATTC CTGTATACGA
251 AATCATAAAA TCTCATAGAT GTATCCTGAG TAGGGCGGGG TACGTGAAAC
301 CCTGTCTGAA TCTGCCCCGGG ACCACCCGTA AGGCTAAATA CTAATCAGAC
351 ACCGATAGTG AACTAGTACC GTGAGGGAAA GGTGAAAAGA ACCCGAGAGG
401 GGAGTGAAAT AGATTCTGAA ACCATTTACT TACAAGTAGT CAGAGCACGT
451 TAAAGTGTGA TGGCGTACAT CTTGCAGTAT GGGCCGGCGA GTTATGTTAA
501 TATGCAAGGT TAAGCACGAA AAAAGCGGAG CCGTAGGGAA ACCGAGTCTG
551 AATAGGGCGA CTTTAGTATA TTGGCATATA CCCGAAACCA GGTGATCATC
601 CATGAGCAGG TTGAAGCTTA GGTA AAACTA AGTGGAGGAC CGAACCGTAG
651 TACGCTAAAA AGTGCCCCGA TGACTTGTGG ATAGTGGTGA AATTCCAATC
701 GAACCTGGAG ATAGCTGGTT CTCTTCGAAA TAGCTTTAGG GCTAGCGTAT
751 AGTACTGTTT AATGGGGGTA GAGCACTGAA TGTGGAATGG CGGCATCTAG
801 CTGTACTGAC TATAATCAAA CTCCGAATAC CATTAAAATT AAGCTATGCA
851 GTCGGAACGT GGGTGATAAC GTCCACGCTC GCGAGGGAAA CAACCCAGAT
901 CCGTCAGCTA AGGTCCCAA ATTGTGTAA GTGAGAAAGG TTGTGGAGAT
951 TTCATAAACA ACTAGGAAGT TGGTTTAGAA GCAGCCACCT TTTAAAGAGT
1001 GCGTAATTGC TCACTAGTCA AGAGATCTTG CGCCAATAAT GTAACGGGAC
1051 TCAAACACAA TACCCAAGCT ACGGGCACAT TATGTGCGTT AGGAGAGCGT
1101 TTTAATTTTCG TTGAAGTCAG ACCGTGAGAC TGGTGGAGAG ATTA AAAAGTT
1151 CGAGAATGCC GGCATGAGTA ACGATTGAA GTGAGAATCT TCGACGCCTA
1201 TTGGGAAAGG TTTCTGGGC AAGGTTCTCC ACCCAGGGTT AGTCAGGGCC
1251 TAAGATGAGG CAGAAATGCA TAGTCGATGG ACAACAGGTT AATATTCCTG

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FIGURE 13B

1301 TACTTGGTAA AAGAATGATG GAGTGACGAA AAAGGATAGT TCTACCACTT
1351 CCACTATGTC CTATCAATAG GAGCTGTATT TGGCATCATA GGAGGCTTCA
1401 TTCACTGATT TCCCCTATTC TCAGGCTACA CCCTAGACCA AACCTACGCC
1451 AAAATCCATT TCACTATCAT ATTCATCGGC GTAAATCTAA CTTTCTTCCC
1501 ACAACACTTT CTCGGCCTAT CCGGAATGAC CCGACCCGAC GTTACTCGGA
1551 CTACCCCGAT GCATACACCA CATGAAACAT CCTATCATCT GTAGGCTCAT
1601 TCATTTCTCT AACAGCAGTA ATATTAATAA TTTTCATGAT TTGAGAAGCC
1651 TTCGCCTTCG AAGCGAAAAG TCCTAATAGT AGAAGAACCC TCCATAAACC
1701 TGGAGTGACT ATATGGATGC CCCCACCCTA CCTCACATTC GAAGAACCCG
1751 TATACATAAA ATCTAGACAA AAAAGGAAGG AAGTGAACGC CCCACAAAAA
1801 AAAAAAAAAA AAAAAAAAAA

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FIGURE 14A

1 AACTAAGTGG AGGACCGAAC CGTAGTACGC TAAAAAGTGC CCGGATGACT
51 TGTGGATAGT GGTGAAATTC CAATCGAACC TGGAGATAGC TGGTTCTCTT
101 CGAAATAGCT TTAGGGCTAG CGTATAGTAT TGTTTAATGG GGGTAGAGCA
151 CTGAATGTGG AATCGGCGGC ATCTAGCTGT ACTGACTATA ATCAAACCTCC
201 GAATACCATT AAAATTAAGC TATGCAGTCG GAACGTGGGT GATAACCTCC
251 ACTCTCGCGA GGGAAACAAC CCAGATCGTC AGCTAAGGTC CCAAATTGT
301 GTTAAGTGAG AAAGGTTGTG AGATTTTATA AACAACTAGG AAGTTGGCTT
351 AGAAGCAGCC ACCTTTTAAA GAGTGCGTAA TTGCTCACTA GTCAAGAGAT
401 CTTGCGCCAA TAATGTAACG GGAATCAAAC ACAATACCGA AGCTACGGGC
451 ACATTATGTC GGTTAGGAGA GCGTTTAAAT TTCGTTGAAG TCAGACCGTG
501 AGACTGGTGG AGAGATTAAA AGTTCGAGAA TGCCCGGCAT GAGTAACGAT
551 TCGAAGTGAG AATCTTCGAC GCCTATTGGG AAAGGTTTCC TGGGCAAGGT
601 TCGTCCACCC AGGGTTAGTC AGGGCCTAAG ATGAGGCAGA AATGCATAGT
651 CGATGGACAA CAGGTTAATA TTCCTGTACT TGGTAAAAGA ATGATGGAGT
701 GACGAAAAAG GATAGTTCTA CCACTTACTG GATTGTGGGG TAAGCAACAA
751 GAGAGTTATA TAGGCAAATC CGTATAGCAT AATCTTGAGT TGTGATGCAT
801 AGTGAAGACT TCGGTCGAGT AACGAATTGA ATCGATTTCA TGTTTCCAAG
851 AAAAGCTTCT AGTGTTAATT TTTTATCAAC CTGTACCGAG AACGAACACA
901 CGTTCCCAAG ATGAGTATTC TAAGGCGAGC GAGAAAACCA ATGTTAAGGA
951 ACTCTGCAAA ATAACCCCGT AAGTTCGCGA GAAGGGGCGC CTATTTTAA
1001 TAGGCCACAG AAAATAGGGG GGCAACTGTT TATCAAAAAC ACAGCTCTCT
1051 GCTAAGTTGT AAAACGACGT ATAGAGGGTG AAGCCTGCCC AGTCCCGAAG
1101 TTAAACGGAG ATGTTAGCTT ACGCAAAGCA TTAAAGTGAA GCCCGGGTGA
1151 ACGGCGGCCG TAACTATAAC GGTCCTAAGG TAGCGAAATT CCTTGTCAAC
1201 TAATTATTGA CCTGCACGAA AGGCGCAATG ATCTCCCTAC TGTCTCAACA
1251 TTGGAATCGG TGAAATTATG GTACCAGTGA AAACGCAGGT TACCCGCATC

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FIGURE 14B

1301 AAGACGAAAA GACCCCGTGG AGCTTTACTA TAACTTCGTA TTGAAAATTG
1351 GTTTAGCATG TGTAGGATAG GCGGGAGACT TTGAAGCTGG GACGCTAGTT
1401 CTAGTGGAGT CAACCTTGAA ATACCACCCT TGCTAAATTG ATTTTCTAAC
1451 CCGTTCCCCT TATCTGGAAG GAGACAGTGC GTGGTGGGTA GTTTGACTGG
1501 GCGGTCGCCT CCTAAAGTGT AACGGAGGCG TTCAAAGCTA CACTCAATAT
1551 GGTCAGAAAC CATATGCAGA GCACAAAGGT AAAAGTGTGG TTGACTGCAA
1601 GACTTACAAG TCGAGCAGGT GCGAAAGCAG GACTTAGTGA TCCGGCGGTA
1651 CATTGTGGAA TGGCCGTCGC TCAACGGATA AAAGTCACCC CGGGGATAAC
1701 AGGCTAATCT TCCCCAAGAG ATCACATCGA CGGGAAGGTT TGGCACCTCG
1751 ATGTCGGCTC ATCGCATCCT GGAGCTGGAG TCGGTTCCAA GGGTTTGCTG
1801 TTCGCCAATT AAAGCGGTAC GTGAGCTGGG TTCAGAACGT CGTGAGACAG
1851 TTCGGTCCTC CACTTAGTT

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FIGURE 15A

- 1 CGGCACGAGC GGCACGAGAG AAGAGACTCC AATCGACAAG
AAGCTGGAAA
- 51 AGAATGATGT TGTCTTAAA CAACCTACAG AATATCATCT
ATAACCCGGT
- 101 AATCCCGTTT GTTGGCACCA TTCCTGATCA GCTGGATCCT
GGAACTTTGA
- 151 TTGTGATACG TGGGCATGTT CCTAGTGACG CAGACAGATT
CCAGGTGGAT
- 201 CTGCAGAATG GCAGCAGCGT GAAACCTCGA GCCGATGTGG
CCTTTCATTT
- 251 CAATCCTCGT TTCAAAGGG CCGGCTGCAT TGTTTGCAAT
ACTTTGATAA
- 301 ATGAAAAATG GGGACGGGAA GAGATCACCT ATGACACGCC
TTTCAAAGA
- 351 GAAAAGTCTT TTGAGATCGT GATTATGGTG CTGAAGGACA
AATTCCAGGT
- 401 GGCTGTAAAT GGAAAACATA CTCTGCTCTA TGGCCACAGG
ATCGGCCAG
- 451 AGAAAATAGA CACTCTGGGC ATTTATGGCA AAGTGAATAT
TCACTCAATT
- 501 GGTTTTAGCT TCAGCTCGGA CTTACAAAGT ACCCAAGCAT
CTAGTCTGGA
- 551 ACTGACAGAG ATAGTTAGAG AAAATGTTCC AAAGTCTGGC
ACGCCCCAGC
- 601 TTAGCCTGCC ATTCGCTGCA AGGTTGAACA CCCCATGGG
CCCTGGACGA
- 651 ACTGTCGTCG TTCAAGGAGA AGTGAATGCA AATGCCAAAA
GCTTTAATGT
- 701 TGACCTACTA GCAGGAAAAT CAAAGGATAT TGCTCTACAC
TTGAACCCAC
- 751 GCCTGAATAT TAAAGCATTT GTAAGAAATT CTTTCTTCA
GGAGTCCTGG
- 801 GGAGAAGAAG AGAGAAATAT TACCTCTTTC CCATTAGTC
CTGGGATGTA

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FIGURE 15B

- 851 CTTTGAGATG ATAATTTATT GTGATGTTAG AGAATTCAAG
GTTGCAGTAA
- 901 ATGGCGTACA CAGCCTGGAG TACAAACACA GATTTAAAGA
GCTCAGCAGT
- 951 ATTGACACGC TGGAAATTAA TGGAGACATC CACTTACTGG
AAGTAAGGAG
- 1001 CTGGTAGCCT ACCTACACAG CTGCTACAAA AACCAAAATA
CAGAATGGCT
- 1051 TCTGTGATAC TGGCCTTGCT GAAACGCATC TCACTGGTCA
TTCTATTGTT
- 1101 TATATTGTTA AAATGAGCTT GTGCACCAT T AGGTCCTGCT
GGGTGTTCTC
- 1151 AGTCCTTGCC ATGACGTATG GTGGTGTCTA GCACTGAATG
GGGAAACTGG
- 1201 GGGCAGCAAC ACTTATAGCC AGTTAAAGCC ACTCTGCCCT
CTCTCCTACT
- 1251 TTGGCTGACT CTTCAAGAAT GCCATTCAAC AAGTATTTAT
GGAGTACCTA
- 1301 CTATAATACA GTAGCTAACA TGTATTGAGC ACAGATTTTT
TTTGGTAAAT
- 1351 CTGTGAGGAG CTAGGATATA TACTTGGTGA AACAAACCAG
TATGTTCCCT
- 1401 GTTCTCTTGA GCTTCGACTC TTCTGTGCGC TACTGCTGCG
CACTGCTTTT
- 1451 TCTACAGGCA TTACATCAAC TCCTAAGGGG TCCTCTGGGA
TTAGTTATGC
- 1501 AGATATTAAA TCACCCGAAG AACTA ACTT ACAGAAGACA
CAACTCCTTC
- 1551 CCCAGTGATC ACTGTCATAA CCAGTGCTCT GCCGTATCCC
ATCACTGAGG
- 1601 ACTGATGTTG ACTGACATCA TTTTCTTTAT CGTAATAAAC
ATGTGGCTCT
- 1651 ATTAGCTGCA AGCTTTACCA AGTAATTGGC ATGACATCTG
AGCACAGAAA
- 1701 TTAAGCCAAA AAACCAAAGC AAAACAAATA CATGGTGCTG
AAATTA ACTT

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FIGURE 15C

- 1751 GATGCCAAGC CCAAGGCAGC TGATTTCTGT GTATTTGAAC
TTACCCGAAA
- 1801 TCAGAGTCTA CACAGACGCC TACAGAAGTT TCAGGAAGAG
CCAAGATGCA
- 1851 TTCAATTTGT AAGATATTTA TGGCCAACAA AGTAAGGTCA
GGATTAGACT
- 1901 TCAGGCATTC ATAAGGCAGG CACTATCAGA AAGTGTACGC
CAACTAAGGG
- 1951 ACCCACAAAG CAGGCAGAGG TAATGCAGAA ATCTGTTTTG
TTCCCATGAA
- 2001 ATCACCAATC AAGGCCTCCG TTCTTCTAAA GATTAGTCCA
TCATCATTAG
- 2051 CAACTGAGAT CAAAGCACTC TTCCACTTTA CGTGATTAAA
ATCAAACCTG
- 2101 TATCAGCAAG TTAAATGGTT CCATTTCTGT GATTTTTCTA
TTATTTGAGG
- 2151 GGAGTTGGCA GAAGTTCCAT GTATATGGGA TCTTTACAGG
TCAGATCTTG
- 2201 TTACAGGAAA TTTCAAAGGT TTGGGAGTGG GGAGGGAAAA
AAGCTCAGTC
- 2251 AGTGAGGATC ATTCCACATT AGACTGGGGC AGAACTCTGC
CAGGATTTAG
- 2301 GAATATTTTC AGAACAGATT TTAGATATTA TTTCTATCCA
TATATTGAAA
- 2351 AGGAATACCA TTGTCAATCT TATTTTTTTA AAAGTACTCA
GTGTAGAAAT
- 2401 CGCTAGCCCT TAATTCTTTT CCAGCTTTTC ATATTAATGT
ATGCAGAGTC
- 2451 TCACCAAGCT CAAAGACACT GGTGTTTTGGT GGAGGGTGCC
ACAGGGAAAG
- 2501 CTGTAGAAGG CAAGAAGACT CGAGAATCCC CCAGAGTTAT
CTTCTCCAT
- 2551 AAAGACCATC AGAGTGCTTA ACTGAGCTGT TGGAGACTGT
GAGGCATTTA
- 2601 GGAAAAAAAT AGCCCACTCA CATCATTCCT TGTAAGTCTT
AAGTTTCAATTT

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FIGURE 15D

- 2651 TCATTTTACG TGGAGGAAAA AAATTTAAAA AGCTATTAGT
ATTTATTAAT
- 2701 GAATTTTACT GAGACATTTT TTAGAAATAT GCACTTCTAT
ACTAGCAAGC
- 2751 TCTGTCTCTA AAATGCAAGT TGGCCTTTTG CTTGCCACAT
TTCTGCATTA
- 2801 AACTTCTATA TTAGCTTCAA AGGCTTTTAA TCTCAATGCG
AACATTCTAC
- 2851 GGGATGTTCT TAGATGCCTT TAAAAAGGGG GCAAGATCTA
ATTTTATTTG
- 2901 AACCCTCACT TTCCAACCTT CACCATGACC CAGTACTAGA
GATTAGGGCA
- 2951 CTTCAAAGCA TTGAAAAAAA TCTACTGATA CTTACTTTCT
TAGACAAGTA
- 3001 GTTCTTAGTT AACCACCAAT GGAAGTGGGT TCATTCTGAA
TCCTGGAGGA
- 3051 GCTTCCTCGT GCCACCCAGT GTTCTGGGC CCTCTGTGTG
AGCAGCCAGG
- 3101 TGTGAGCTGT TTTAGAAGCA GCGTGTGTC TTCATCTCTC
CCGTTTCCCA
- 3151 AAAGAACAAA GGATAAAGGT GACAGTCACA CTCCTGGGTT
AAAAAAAGCA
- 3201 TTCCAGAACC ACTTCTCTTT ATGGGCACAA CAACAAAGAA
GCTAAGTTCTG
- 3251 CCTACCCAAA TGAAAGTAGG CTTTACAGTC AAGTACTTCT
GTTGATTGCT
- 3301 AAATAACTTC ATTTTCTTGA AATAGAGCAA CTTTGAGTGA
AATCTGCAAC
- 3351 ATGGATACCA TGTATGTAAG ATACTGCTGT ACAGAAGAGT
TAAGGCTTAC
- 3401 AGTGCAAATG AGGCGTCAGC TTTGGGTGCT AAAATTAACA
AGTCTAATAT
- 3451 TATTACCATC AATCAGGAAG AGATAATAAA TGTTTAAACA
AACACAGCAG
- 3501 TCTGTATAAA AATACGTGTA TATTTACTCT TTCTGTGCAC
GCTCTATAGC

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FIGURE 15E

- 3551 ATAGGCAGGA GAGGCTTATG TGGCAGCACA AGCCAGGTGG
GGATTTTGTA
- 3601 AAGAAGTGAT AAAACATTG TAAGTAATCC AAGTAGGAGA
TATTAAGGCA
- 3651 CCAAAAGTAA CATGGCACCC AACACCCAAA AATAAAAATA
TGAAATATGA
- 3701 GTGTGAACTC TGAGTAGAGT ATGAAACACC ACAGAAAGTC
TTAGAAATAG
- 3751 CTCTGGAGTG GCTCTCCCAG GACAGTTTCC AGTTGGCTGA
ATAGTCTTTT
- 3801 GGCAGTGATG TTCTACTTCT TCACATTCAT CTAATAAATA
AAAAAAAAAA

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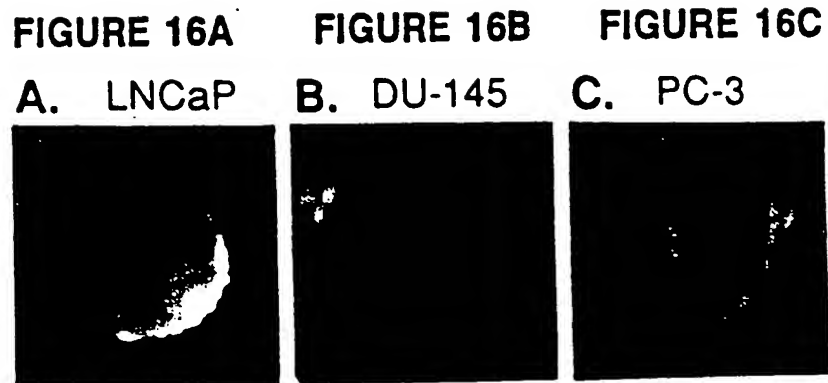
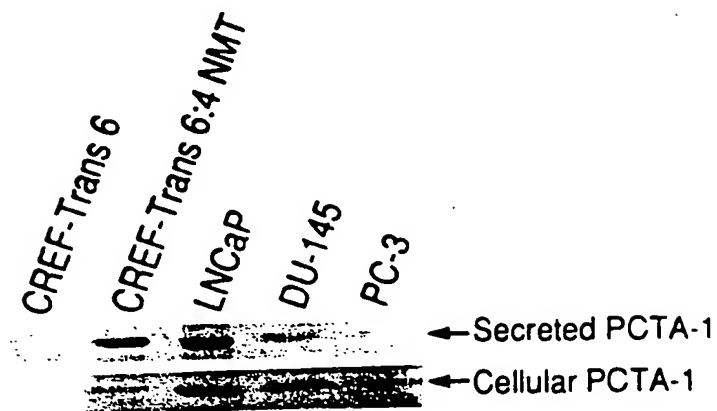


FIGURE 16D Secreted and Cellular PCTA-1



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FIGURE 17A

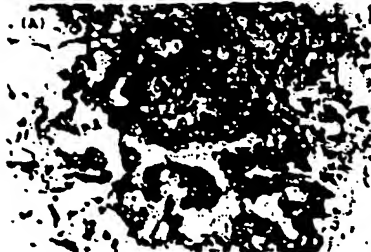


FIGURE 17E

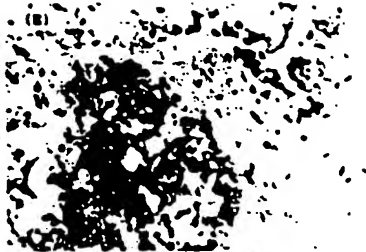


FIGURE 17B



FIGURE 17F



FIGURE 17C



FIGURE 17G



FIGURE 17D



FIGURE 17H



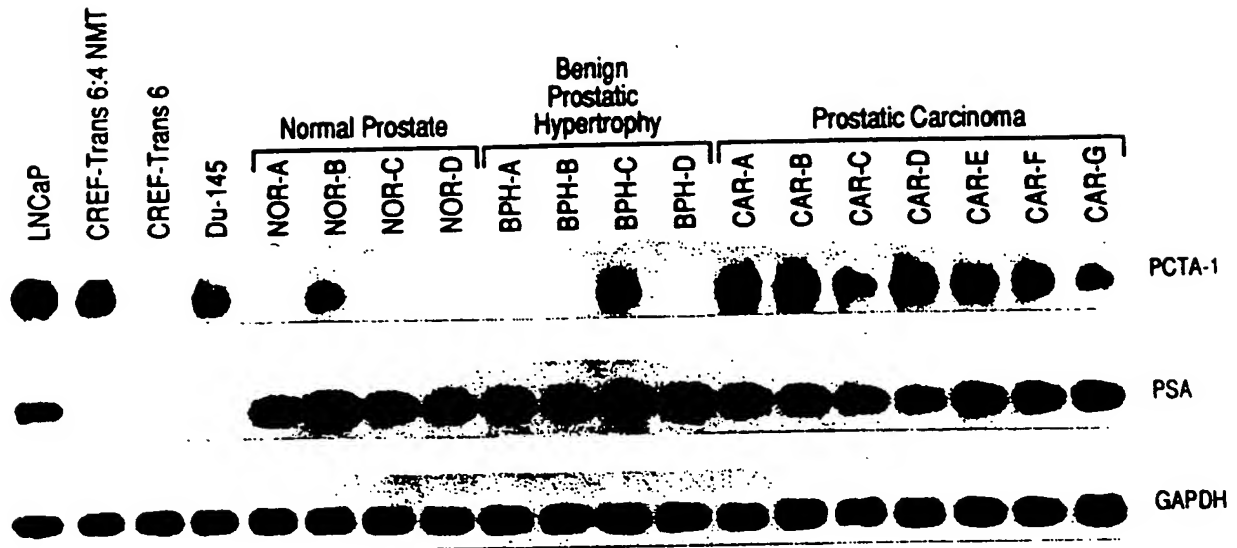
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FIGURE 18A

54 ATG ATG TTG TCC TTA AAC AAC CTA CAG AAT ATC ATC TAT AAC CCG GTA ATC CCG TTT GTT
 M L S L N N L Q N I I Y N P V I P F V
 114 GGC ACC ATT CCT GAT CAG CTG CAG CCT GAT CCT GAT CAG CTG ATA CCG CAT GTT CCT
 G T I P D Q L L P G T L I V I R G H V P
 174 AGT GAC GCA GAC AGA TTC CAG GTG GAT CTG CAG AAT GGC AGC AGC GTG AAA CCT CGA GCC
 S D A D F Q Q CCG TTT CAG GAA GAG ATC ACC TAT GAC AGC CCT TTC AAA AGA GAA
 234 GAT GTG GCC TTT CAT TTT AAT CCG TTT CAG AAT GGC GGC TGC ATT GTT TGC AAT ACT
 D V A F F N G TGG GGA GAG E I T Y D T P F K R C N T
 294 TTG ATA AAT GAA AAA TGG GGA CCG GAA GAG ATC ACC TAT GAC AGC CCT TTC AAA AGA GAA
 L I N E K W G I V I M V L K D K F Q V A V N G
 354 AAG TCT TTT GAG ATC GTG ATT ATG GTG CTG AAG GAC AAA TTC CAG GTG GCT GTA AAT GGA
 K S F E I V I G R I G P E K I D T L G I
 414 AAA CAT ACT CTG CTC TAT GGC CAC AGG ATC GGC CCA GAG AAA ATA GAC ACT CTG GGC ATT
 K H T L L Y G G H R I G P E K I D T L G I
 474 TAT GGC AAA GTG AAT ATT CAC TCA ATT GGT TTT AGC TTC AGC TCG GAC TTA CAA AGT ACC
 Y G G K V N I H S I G F S F S D L Q S T
 534 CAA GCA TCT AGT CTG GAA CTG ACA GAG ATA GTT AGA GAA AAT GTT CCA AAG TCT GGC ACG
 Q A S S L E L T E I V R E N V P K S G T
 594 CCC CAG CTT AGC CTG CCA TTC GCT GCA AGG TTG AAC ACC CCC ATG GGC CCT GGA CGA ACT
 P Q L S L P F A A R L N T P M G P G R T
 654 GTC GTC GTT CAA GGA GAA GTG AAT GCA AAT GCC AAA AGC TTT AAT GTT GAC CTA CTA GCA
 V V V Q G E V N A N A K S F N V D L L A
 714 GGA AAA TCA AAG GAT ATT GCT CTA CAC TTG AAC CCA CGC CTG AAT ATT AAA GCA TTT GTA
 G K S K D I A L H L N P R L N I K A F V
 774 AGA AAT TCT TTT CAG GAG TCC TGG GGA GAA GAG AGA AAT ATT ACC TCT TTC CCA
 R N S F L Q E S W G E E R N I T S F P
 834 TTT AGT CCT GGG ATG TAC TTT GAG ATG ATA ATT TAT TGT GAT GTT AGA GAA TTC AAG GTT
 F S P G M Y F E M I I Y C D V R E F K V
 894 GCA GTA AAT GGC GTA CAC AGC CTG GAG TAC AAA CAC AGA TTT AAA GAG CTC AGC AGT ATT
 A V N G V H S L E Y K H R F K E L S S I
 954 GAC ACG CTG GAA ATT AAT GGA GAC ATC CAC TTA CTG GAA GTA AGG AGC TGG TAG
 D T L E I N G D I H L L L E V R S W

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FIGURE 19



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